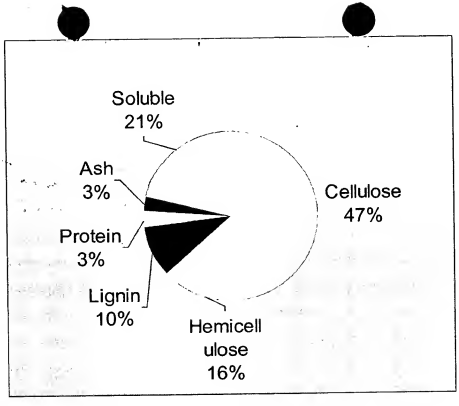


Figure 1.

10080114-022102

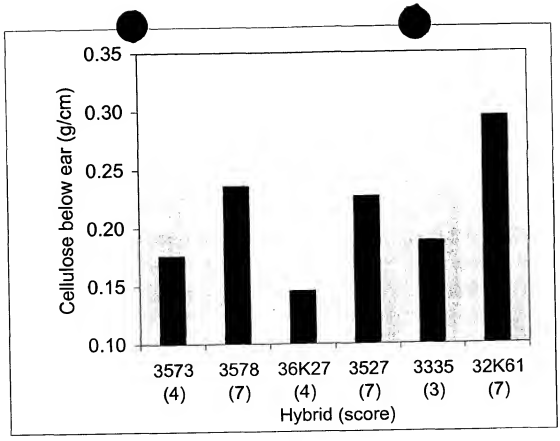


Figure 2

20120214-US-100801

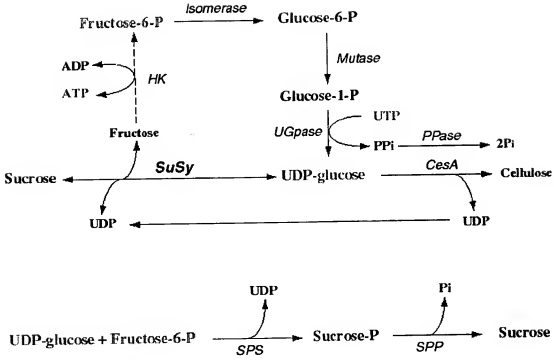


Figure 3.

10080114 - 021102

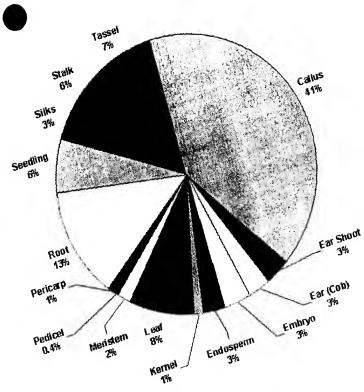


Figure 4.

10080114.022102

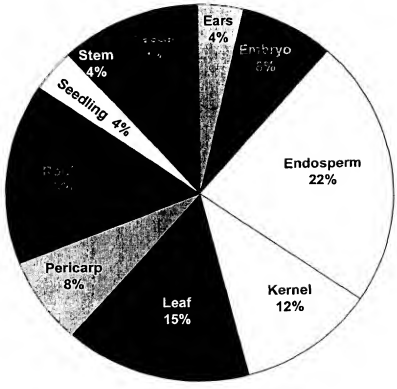


Figure 5

10080114.022102

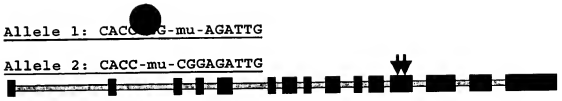


Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
Sus-1 (WT)	63.2	25.2 +/-0.38	39.9
sus-1 (mutant)	47.3	17.7 +/-0.34	37.4

1008014.02102

```
                    1                                                  50
      Sh1     (1)  -----MAAKLTRLHSLRERIGATFSSHPNELIALFSRYVHQGKGMLQRHQ
      Sus1    (1)  MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFPTRLKNLGKGMLQPHQ
      Sus3    (1)  ----------STHASGDRVEDTLHAHRNELVALLSKYVNKGKGILQPHH
Consensus     (1)            LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ
                    51                                                 100
      Sh1    (46)  LLAEFD-ALFDSDKE--KYAPFEDILRAAQEAIVLFPWVALAIRPRPGVW
      Sus1   (51)  ILAEYNNALFEAEREKLKDGAFEDVLRAAQEAIVIFPWVALAIRPRPGVW
      Sus3   (40)  ILDALDEVQGSGGRA-LAEGPFELDVLRSAQEAIVLPPFVAIAVRPRPGVW
Consensus    (51)  ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPPWVALAIRPRPGVW
                    101                                                150
      Sh1    (93)  DYIRVNVSELAVRELSVSEYLAFKEQLVDGQSNSNFVLRLDFEPFNASPF
      Sus1  (101)  EYVRVNVSELAVRELRVPEYLQFKEQLVEGPNNNFVLELDFEPFNASPF
      Sus3   (89)  EYVRVNVHELSVRQLTVSEYLRFKEQLVDGQHNDFVLELDFEPFNVSVF
Consensus   (101)  EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEPFNASPF
                    151                                                200
      Sh1    (143)  RPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAFNYKGTTMMLN
      Sus1   (151)  RPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFIRAFNYKGMTMMLN
      Sus3   (139)  RPNRSSSIGNGVQFLNRHLSSIMFRNRDCLEPLLDFLRGHPHKGHVMMLN
Consensus    (151)  RPSLSKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN
                    201                                                250
      Sh1    (193)  DRIQSLRGLQSSLRKAEEYLLSVPQDTPYSEFNHRFQRLGLEKGWGDTAK
      Sus1   (201)  DRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQRLGLEKGWGDQAK
      Sus3   (189)  DRIQSLGRLQSVLTKAEEHLSKLPADTPYSQFAYKFQEWGLEKGWGDTAG
Consensus    (201)  DRIQSL ALQSALRKAEEHLSSLPADTPYSEF HRFQELGLEKGWGDTAK
                    251                                                300
      Sh1    (243)  RVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLG
      Sus1   (251)  RAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLG
      Sus3   (239)  HVLEMIHLLLDIIQAPDPSTLEKFLGRIPMIFNVVVVSPHGYFGQANVLG
Consensus    (251)  RVLETIHLLLDLLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG
                    301                                                350
      Sh1    (293)  YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAAGT
      Sus1   (301)  YPDTGGQVVYILDQVRAMENEMLLRIKQQGLDITPKILIVTRLLPDATGT
      Sus3   (289)  LPDTGGQIVYILDQVRALENEMVLRLKQQGLDVSPKILIVTRLIPDAKGT
Consensus    (301)  YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT
                    351                                                400
      Sh1    (343)  TCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEDVS
      Sus1   (351)  TCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVA
      Sus3   (339)  SCNQRLERISGTQHTYILRVPFRNENGILKKWISRFDVWPYLETFAEDAA
Consensus    (351)  TCGQRLEKVIGTEHTHILRVPFRNENGILRKWISRFDVWPYLETYTEDVA
                    401                                                450
      Sh1    (393)  SETMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPN
      Sus1   (401)  HETAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPN
      Sus3   (389)  GEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPD
Consensus    (401)   EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN
                    451                                                500
      Sh1    (443)  SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYE
      Sus1   (451)  SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYE
      Sus3   (439)  SDIFWKNFDEKYHFSCQFTADIIAMNNADFIITSTYQEIAGSKNTVGQYE
Consensus    (451)  SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE
                    501                                                550
      Sh1    (493)  SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYTETDKRLTAFH
      Sus1   (501)  SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH
      Sus3   (489)  SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSLH
Consensus    (501)  SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH
```

Figure 8a

10801414 - 062402

```
                551                                                 600
      Sh1   (543) PEIEELIIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKN
      Sus1  (551) PEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN
      Sus3  (539) GSIENLIYDPEQNDEHIGHLDDRSKPILFSMARLDRVKNITGLVEAFAKC
Consensus   (551) PEIEELIYS  ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN


                601                                                 650
      Sh1   (593) ARLRELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWIS
      Sus1  (601) KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMPDLIEQYNLNGHIRWIS
      Sus3  (589) AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFGQFRWIS
Consensus   (601) ARLRELVNLVVVAGDHG   SKDREEQAEFKKMHDLID YNL GHIRWIS
                651                                                 700
      Sh1   (642) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCH
      Sus1  (650) AQMNRVRNGELYRYICDTKGAFVQPAFVEAFGLTVVEAMTCGLPTFATAV
      Sus3  (639) AQTNRARNGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLH
Consensus   (651) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFAT H
                701                                                 750
      Sh1   (692) GGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQGGL
      Sus1  (700) GGPAEIIVHGVSGYHIDPYQGDKASALLVDFFDKCQAEPSHWSKISQGGL
      Sus3  (689) GGPAEIIEHGVSGFHIDPYHPEQAVNLMADFFDRCKQDPDHWNTISQAGL
Consensus   (701) GGPAEIIVHGVSGFHIDPYH DKAA LLVDFFDKCKADPSHW  ISQGGL
                751                                                 800
      Sh1   (742) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFMALKYR
      Sus1  (750) QRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLVALKYR
      Sus3  (739) QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR
Consensus   (751) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR
                801          817
      Sh1   (792) SLASQVPLSFD------
      Sus1  (800) TMASTVPLAVEGEPSSK
      Sus3  (789) ELAKTVPLAID-QPQ--
Consensus   (801) SLASTVPLAID  P
```

Figure 8b

10080114.022102

10080114.022102

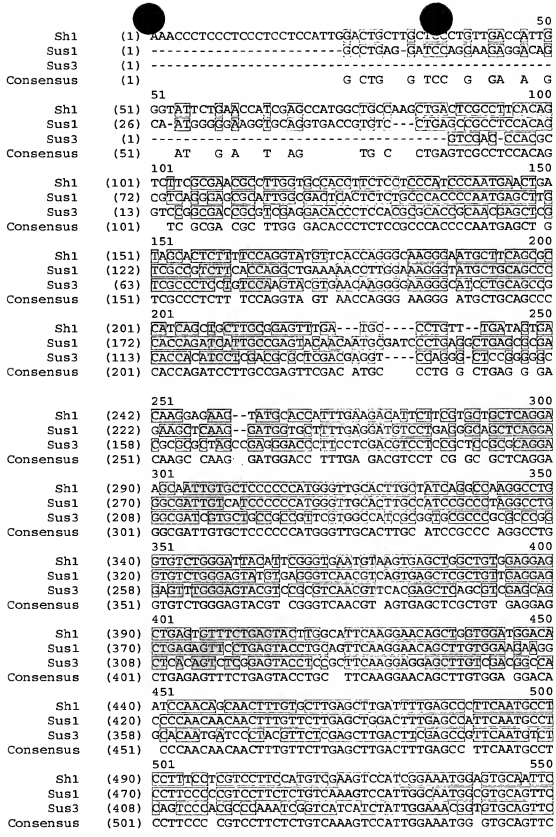


Figure 9a

```
                551                                                   600
Sh1       (540) CTTAACCGACACCTGTCGTCCAAGTTGTTCCAGGACAAGGAGAGTTTGTA
Sus1      (520) CTCAACAGGCACCTGTCATCAAAGCTCTTCCATGACAAGGAGAGCATGTA
Sus3      (458) CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGGA
Consensus (551) CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA
                601                                                   650
Sh1       (590) CCCCTTGCTGAACTTCCTCAAGGCTCATAACTACAAGGGCACGACGATGA
Sus1      (570) CCCCTTGCTCAACTTCCTTGCGCCCACAACTACAAGGGGATGACCATGA
Sus3      (508) GCCCCTGTTGGATTCCTCCGTGGCCACCGGCACAAGGGGCATGTTATGA
Consensus (601) CCCCTTGCTGAACTTCCTCCG GCCCACAACTACAAGGGGA GAC ATGA
                651                                                   700
Sh1       (640) TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATGCCTGAGA
Sus1      (620) TGTTGAACGACAGAATCCGCAGTCTCAGTGCTCTGCAAGGTGCGCTGAGG
Sus3      (558) TGCTTAATGATAGAATACAAAGTTGGGGAGGCTTCAGTCTGTGCTGACC
Consensus (651) TGTTGAATGACAGAATCCAAAGCCT  GTGGTCT CAATCTGCGCTGAG
                701                                                   750
Sh1       (690) AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA
Sus1      (670) AAGGCTGAGGAGCACCTGTCCACCCTACAAGCTGATACCCCATACTCTGA
Sus3      (608) AAAGCTGAGGAGCAGTTGTGAAAGCTCCCTGCTGACACACCATACTCACA
Consensus (701) AAGGCTGAGGAGCACCTGTC A  CT CCTGCTGACAC CCATACTC GA
                751                                                   800
Sh1       (740) GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGACA
Sus1      (720) ATTTCACCACAGGTTCCAGGAACTTGGTCTGGAGAAGGGTTGGGGTGATT
Sus3      (658) ATTTGCTTATAAATTTCAAGAGTGGGGCCTGGAGAAAGGTTGGGGTGATA
Consensus (751) ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA
                801                                                   850
Sh1       (790) GTGCGAAGCGTGTTCTCGACACACTCCACTTGCTTCTCGACCTTCTTGAG
Sus1      (770) GCGCTAAGCGTGCAGAGCAGACTATCCACCTCCTCTTGGACCTCCTGGAG
Sus3      (708) CAGCAGGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCATTCAG
Consensus (801) C GC AAGCGTGTTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG
                851                                                   900
Sh1       (840) GCCCCTGATCGTGCCAACTTGGAGAAGTTCCTTGGAACTATACCAATGAT
Sus1      (820) GCCCCAGATCCGTCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGGT
Sus3      (758) GGCCCAGACCCATGTACCCTAGAGAAATTCTTGGGGACGATCCCCATGAT
Consensus (851) GCCCCAGATCC TCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGAT
                901                                                   950
Sh1       (890) GTTCAACGTTGTTATCCTGTGTCCTCATGGCTACTTCGCCCAGTTCAATG
Sus1      (870) GTTCAATGTCGTTATCCTCTCCCCTCATGGTTACTTCGCTCAAGCTAATG
Sus3      (808) TTTTAACGTTGTTGTGGGTATCCCCTCATGGATACTTTGGTCAAGCTAATG
Consensus (901) GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG
                951                                                  1000
Sh1       (940) TGCTTGGATACCCTGACACTGGCGGTCAGGTTGTGTACATTCTGGATCAA
Sus1      (920) TCTTGGGTTACCCTGACACCGGAGGCCAGGTTGTCTACATCTTGGATCAA
Sus3      (858) TATTAGGCTTGCCAGACACAGGAGGACAGATCGTCTATATACTGGACCAA
Consensus (951) T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA
               1001                                                  1050
Sh1       (990) GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT
Sus1      (970) GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT
Sus3      (908) GTCCGTGCACTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGGCT
Consensus (1001) GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT
               1051                                                  1100
Sh1       (1040) TGATATCAGTCCGAAGATCCTCATTGTTACCAGGCTGTTGCCTGATGGTG
Sus1      (1020) TGACATCAGGCCGAAGATCCTATTGTCACCAGGTTGCTCCCTGATGCAA
Sus3      (958) TGATGTTTCCCCAAAGATTCTCATTGTTACTCGGCTGATACCAGATGCAA
Consensus (1051) TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA
```

Figure 9b

20210114.0210

```
                1101                                                1150
Sh1       (1090) CTGGGACTACGTGCGGTCAGCGGCTGGAGAAGGTCATTGGTACTGAGCAC
Sus1      (1070) CTGGCACCACCTGTGGCCAGCGCCTTGAGAAGGTCCTTGGCACCGAGCAC
Sus3      (1008) AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAACACAGCAT
Consensus (1101) CTGG AC AC TGCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC
                1151                                                1200
Sh1       (1140) ACAGACATCATTCGCGTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA
Sus1      (1120) TGCCATATCGCTTCGCGTGCGATTCAGAACAGAAAACGGAATCGTTCGCAA
Sus3      (1058) ACTTACATATTACGAGTTCCCTTCAGAAATGAAAATGGGATACTTAAGAA
Consensus (1151) AC  ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA
                1201                                                1250
Sh1       (1190) GTGGATCTCTCGTTTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
Sus1      (1170) GTGGATCTCGCGATTTGAAGTCTGGCCGTACCTGGAGACGTTACACTGATG
Sus3      (1108) ATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGG
Consensus (1201) GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
                1251                                                1300
Sh1       (1240) ATGTTTTCCAGTGAAATAATGAAAGAAATGCAGGCCAAGCCTGACCTTATC
Sus1      (1220) ACGTGGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC
Sus3      (1158) ATGCTGGTGGTGAAATTGCTGCTGAATTTACAAGGTACTCCAGACTTCATA
Consensus (1251) ATGTTGC  GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC
                1301                                                1350
Sh1       (1290) ATTGGCAACTACAGCGATGGCAACCTAGTCGCCACCTCTGCTCGGCACAA
Sus1      (1270) ATCGGAAACTACAGTGACGGAAACCTTGTTGCGTGTTTGCTCGCCCACAA
Sus3      (1208) ATTGGAAACTACAGTGATGGAAATCTTGTGGCGTCATTGCTATCTTACAA
Consensus (1301) ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGCTCGC CACAA
                1351                                                1400
Sh1       (1340) GTTGGGAGTCACTCAGTGTACCATCGCTCATGCCTTGGAGAAAACCAAAT
Sus1      (1320) GATGGGTGTTACTCACTGTACCATTGCCCATGCGCTTGAGAAAACTAAGT
Sus3      (1258) GATGGGAATTACCCAGTGCAACATTGCTCATGCTCTGGAAAAGACTAAGT
Consensus (1351) GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACTAAGT
                1401                                                1450
Sh1       (1390) ACCCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACTTC
Sus1      (1370) ACCCTAACTCCGACCTCTACTGGAAGAAGTTTGAGGATCACTACCACTTC
Sus3      (1308) ATCCAGATTCAGACATAATTTGGAAGAATTTCGATGAGAAGTACCATTTC
Consensus (1401) ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC
                1451                                                1500
Sh1       (1440) TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCACCGATTTCAT
Sus1      (1420) TCGTGCCAGTTCACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT
Sus3      (1358) TCCTGCCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT
Consensus (1451) TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT
                1501                                                1550
Sh1       (1490) CATCACCAGCACATTCCAAGAAATCGCGGGAAGCAAGGACACCGTGGGGC
Sus1      (1470) CATCACCAGTACCTTCCAAGAGATCGCCGGAAACAAGGACACCGTCGGCC
Sus3      (1408) CATCACCAGCACATACCAAGAAATTGCTGGAAGCAAAAATACTGTTGGAC
Consensus (1501) CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C
                1551                                                1600
Sh1       (1540) AGTACGAGTCCCATATCGCGTTCACTCTTCCTGGCCTCTACCGTGTCGTC
Sus1      (1520) AGTACGAGTCACACATGGCGTTCACAATGCCTGGCCTGTACCGCGTTGTC
Sus3      (1458) AGTATGAGAGTCATACTGGCTTTACTCTGCCTGGTCTGTACCGAGTTGTC
Consensus (1551) AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC
                1601                                                1650
Sh1       (1590) CATGGCATCGATGTTTTCGATCCCAAGTTCAACATTGTCTCTCCTGGAGC
Sus1      (1570) CACGGCATTGATGTCTTCGACCCCAAGTTCAACATCGTGTCTCCTGGCGC
Sus3      (1508) CATGGGATCGATGTCTTCGATCCAAAGTTCAATATAGTCTCTCCTGGAGC
Consensus (1601) CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC
```

Figure 9c

10080414.021102

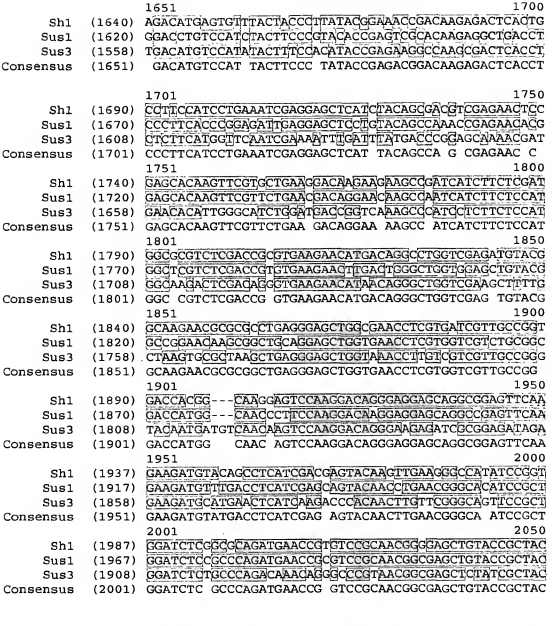
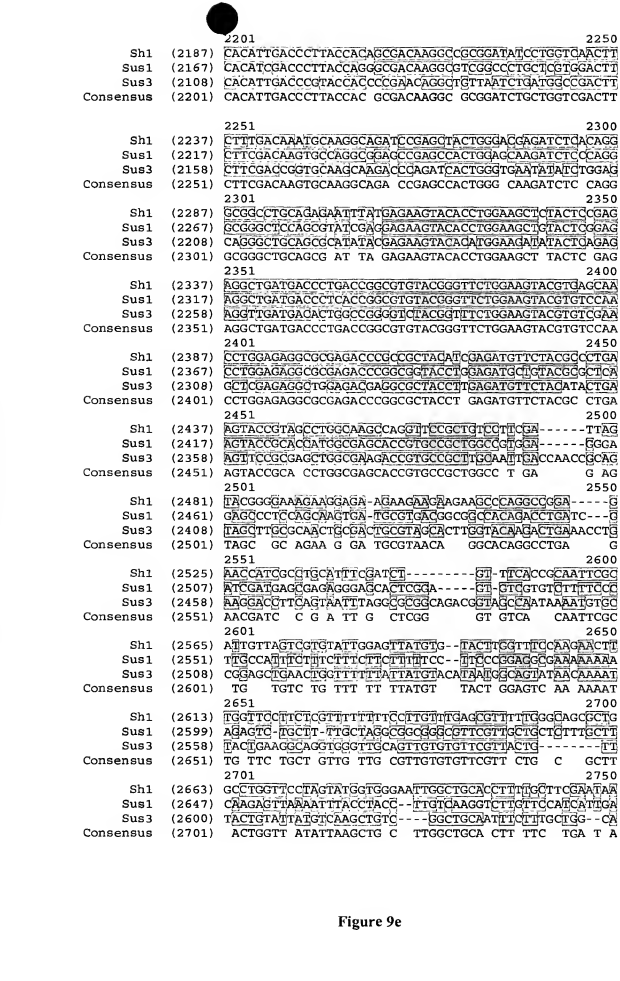


Figure 9d



10030114.022102

Figure 9e

```
                2751                                                2800
      Sh1  (2713) AAATGCCTGCTCGTTCACCTGTCTTCCAGAGTGC----------------
      Sus1 (2695) TCCGGGTGTCTCGCTTGTAGTAGTCTGATGGACTGTTAGTAGTTTGCGTTGC
      Sus3 (2644) AGCCGCAGGCACTGGTGAAGTGCTGATAAATACATCATATTCTGTTGACC
Consensus  (2751) A C GC GGC CTTGTA   GTCTGATAGA TG T  TA T TG     C
                2801                                                2850
      Sh1  (2747) ----------------------------------------------------
      Sus1 (2745) GTCGGTTGAGAGGGAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
      Sus3 (2694) TGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGGCCGC------
Consensus  (2801)    G    A A   AA                   G G G    C

                2851                                                2900
      Sh1  (2747) ----------------------------------------------------
      Sus1 (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
      Sus3 (2738) ----------------------------------------------------
Consensus  (2851)
                2901                                                2950
      Sh1  (2747) ----------------------------------------------------
      Sus1 (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
      Sus3 (2738) ----------------------------------------------------
Consensus  (2901)
                2951      2964
      Sh1  (2747) --------------
      Sus1 (2895) ACCTTTGCAGCTGT
      Sus3 (2738) --------------
Consensus  (2951)
```

Figure 9f

10080114.022102

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG

CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCATGTCTGCCCCGAAGCTGA

ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC

TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA

TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT

TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

10080114.022102

Sorghum sequenc[redacted]m SEQ ID NO: 13 in SEQ ID NO: 11

ATGTCTGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

[redacted]accgcgtcga ggacaccctc cacgcgcacc gcaacgagct 60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat 120
cctcgacgcg ctcgacgagg tccagggctc cgggggccgc gcgctagccg agggaccctt 180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc 240
ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt 300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca 360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc 420
aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat 480
catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca 540
caaggggcat gttatgatgc ttaatgatag aatacaaagc ttgggggagc ttcagtctgt 600
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Figure 11

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